

Jarrell, Noble

186188

**From:** Ramirez, Delia  
**Sent:** Wednesday, April 19, 2006 6:24 PM  
**To:** Jarrell, Noble  
**Subject:** 10/665455

Hi,

I would like to request the following alignments: SEQ ID NO:1 against SEQ ID NO:2-7.

Thank you very much,

---

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Noble  
ST/Fm 4/23/06  
Gen ID 19g  
SPR  
SUN 7N/A

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# Sim

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## Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (177 residues)

## using the parameters:

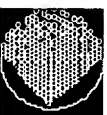
*Seq 1D NO:1 VS Seq 1D NO:2  
(PROTEIN TRANSLATION)*

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.9% identity in 177 residues overlap; Score: 927.0; Gap frequency: 0.0%

UserSeq1, 1 MPLEKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER

UserSeq2, 1 MPLEKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER

\*\*\*\*\*

4

42

UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMSLKGVLVKVRPTELDIDKEYG  
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMSLKGVLVKVRPTELDIDKEYG  
\*\*\*\*\*

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRG  
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRG  
\*\*\*\*\*

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG  
UserSeq2, 148 VCWTVLG  
\* \* \*\*

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG  
UserSeq2, 136 ICQTDLG  
\* \* \*\*

---

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL  
UserSeq2, 154 GYACAYSSAFMGREI  
\*\* \* \*

---

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI  
UserSeq2, 69 GYQSGLKDAELARKL

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## Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

## using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

Seq ID NO:1 VS Seq ID NO:3



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

```

UserSeq1,      1  MPTAEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER
UserSeq2,      1  MPISKYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQFSAMASFRREMTNTLGIER
***          *****

```

4

42

112

```
UserSeq1,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPT112ELDIDKEYG
UserSeq2,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTGLDIDKEYG
*****
UserSeq1,     121 RFYAEMEWIDWFEEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
UserSeq2,     121 RFYAEMEWIDWFEEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
*****
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,      136 ICQTDLG
UserSeq2,      148 VCWTVLG
* * * *
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,      148 VCWTVLG
UserSeq2,      136 ICQTDLG
* * * *
```

---

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      69 GYQSGLKDAELARKL
UserSeq2,     154 GYACAYSSAFMGREI
** * *
```

---

33.3% identity in 9 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      82 KLRPNASEV
UserSeq2,     107 KVRPTGLDI
```

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### Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

Seq ID No: 1 VS Seq ID No: 4

### using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.8% identity in 180 residues overlap; Score: 938.0; Gap frequency: 0.0%

UserSeq1,  
UserSeq2,

1 MPEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNLGIER  
1 MPKIKPEIRHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNLGIER  
\*\*\*\*\*

4 10

42

117

```
UserSeq1,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
UserSeq2,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDMEYG
*****
UserSeq1,     121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG
UserSeq2,     121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG
*****
```

---

36.4% identity in 11 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
UserSeq1,      82 KLRPNASEVGM
UserSeq2,     107 KVRPTELDIDM
* * *
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,     136 ICQTDLG
UserSeq2,     148 VCWTVLG
* * *
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,     148 VCWTVLG
UserSeq2,     136 ICQTDLG
* * *
```

---

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      69 GYQSGLKDAELARKL
UserSeq2,     154 GYACAYSSAFMGREI
```

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### Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

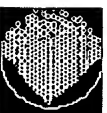
### using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 936.0; Gap frequency: 0.0%

UserSeq1,  
UserSeq2,

1 MPEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGAE  
1 MPKIKKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGAE

\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*

4

42

58

SEQ ID NO:1 VS SEQ ID NO:5



UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHS�KGLVKVRPTELDIDKEYG  
UserSeq2, 61 TKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHS�KGLVKVRPTELDIDKEYG  
\*\*\*\*\*

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMOPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG  
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMOPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG  
\*\*\*\*\*  
140

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG  
UserSeq2, 148 VCWTVLG  
\* \* \* \*

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG  
UserSeq2, 136 ICQTDLG  
\* \* \* \*

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL  
UserSeq2, 154 GYACAYSSAFMGREI  
\* \* \* \*

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI  
UserSeq2, 69 GYQSGLKDAELARKL

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## Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

## using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

Seq ID n.1 VS Seq ID n.2



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 932.0; Gap frequency: 0.0%

UserSeq1,

1 M P I E Y K K P E I Q H S D F K D L T N L I H F Q S M E G K I W L G E Q R M L L L Q S S A M A S F R R E M V N T L G I E R

UserSeq2,

1 M P I K Y K P E I Q H S D F K D L T N L I H F Q S M E G K I W L G E Q R M L L L Q S S A M A S F R R E M V N T L G I E R

\*\*\*\*\*

4

42

116-117

```
UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHS�KGLVKVRPTELDIDKEYG
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHS�KGLVKVRPTELDIDGREYG
*****

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGG
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSALMGREIIFKEVSCRGGG
*****
103
```

---

40.0% identity in 10 residues overlap; Score: 26.0; Gap frequency: 0.0%

```
UserSeq1, 82 KLRPNASEVG
UserSeq2, 107 KVRPTELDIG
* * *
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * *
```

---

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * *
```

---

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL
```

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### Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

seq 1 D N0:1 VS seq 1 D N0:7

### using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

UserSeq1, 1 MPTIEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER  
 UserSeq2, 1 MPITYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER

\*\*\*\*\*  
 \*\*\*\*\*

4

42

UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSCLKGLVKVRPTELDIDKEYG  
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSCLKGLVKVRPTELDIDKEYG  
\*\*\*\*\*

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLDGQMOPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGG  
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLPQMODPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGG  
\*\*\*\*\*

141

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG  
UserSeq2, 148 VCWTVLG  
\* \* \* \*

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI  
UserSeq2, 69 GYQSGLKDAELARKL  
\* \* \* \*

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL  
UserSeq2, 154 GYACAYSSAFMGREI  
\* \* \* \*

33.3% identity in 9 residues overlap; Score: 20.0; Gap frequency: 0.0%

UserSeq1, 107 KVRPTELDI  
UserSeq2, 82 KLRPNASEV